

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:19:03 ; Search time 181 Seconds  
(without alignments)

1496.629 Million cell updates/sec

Title: US-10-628-432-32

Sequence: 2859 1 MSQTSHPGRGLAGRLMGA.....DQLDFNIPOAVDYKDDDDK 529

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2805	98.1	837	1	ATSA_HUMAN
2	2798	97.9	837	2	Q6UWAB
3	2790	97.6	837	2	O6P4Q8
4	2557	89.4	839	2	Q7YS95
5	2460	86.0	845	2	Q8BNJ2
6	2459	86.0	845	2	Q8BNJ2
7	2248	78.6	893	2	Q8K384
8	1659	58.0	339	2	Q8NEK2
9	1613	56.4	630	1	ATSA_RAT
10	1222	42.7	968	1	ATSI_MOUSE
11	1221.5	42.7	967	1	ATSI_MOUSE
12	1220.5	42.7	967	2	O6BEJ2
13	1193	41.7	967	1	ATSI_HUMAN
14	1193	41.7	967	2	O6BEJ2
15	1108	38.8	245	1	ATSA_BOVIN
16	1095	38.3	950	1	ATIS_HUMAN
17	1084	37.9	203	2	Q8CH80
18	1061	37.1	192	2	Q8CH80
19	1053.5	36.8	890	1	ATSA_HUMAN
20	1049.5	36.7	759	2	Q8H2M8
21	1011.5	35.4	905	1	ATSA_MOUSE
22	858	30.0	1906	1	ATSA_MOUSE
23	847	29.6	867	2	Q6K3K3
24	837.5	29.3	930	2	Q6K3K3
25	830.5	29.0	928	2	Q6K3K3
26	827	28.9	930	2	Q6K3K3
27	822	28.8	1935	1	ATSA_HUMAN
28	786	27.5	1911	1	ATSA_HUMAN
29	706.5	24.7	2165	1	Q19791
30	650.5	22.8	997	1	ATSI_HUMAN
31	649.5	22.7	1686	2	Q6P7J9

32	646	22.6	623	2	Q8BGP4	Q8BGP4 m. mus. muscu
33	642	22.5	1641	2	Q6BSA9	Q6BSA9 mus. muscu
34	637	22.3	1593	1	AT12_HUMAN	AT12_HUMAN
35	635	22.2	117	2	Q8VHK4	Q8VHK4 mus. sapien
36	608	21.3	1009	2	Q8BKX1	Q8BKX1 m. mus. muscu
37	608	21.3	1600	2	Q8B1B3	Q8B1B3 mus. muscu
38	598.5	20.9	1095	1	AT17_HUMAN	AT17_HUMAN
39	570	19.9	1077	1	AT10_HUMAN	AT10_HUMAN
40	565.5	19.8	988	2	Q7PWT7	Q7PWT7 homo. sapien
41	564	19.7	1070	2	Q8CG28	Q8CG28 mus. sapien
42	561.5	19.6	769	2	Q8WRU5	Q8WRU5 mus. muscu
43	560.5	19.6	1221	2	Q6PAR5	Q6PAR5 drosophila
44	555.5	19.4	1059	2	Q9W493	Q9W493 drosophila
45	550	19.2	1081	1	AT18_HUMAN	AT18_HUMAN

## ALIGNMENTS

RESULT 1  
ID ATSA\_HUMAN STANDARD; PRT; 837 AA.  
AC 075173; Q9UN83;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE ADAMTS-4 precursor (EC 3.4.24.82) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1) (ADMP-1).  
GN Name=ADAMTS4; Synonyms=K1RA0688;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98403880; PubMed=9734811;  
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";  
RL DNA Res. 5:169-176(1998).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99286303; PubMed=10356395; DOI=10.1126/science.284.5420.1664;  
RA Tortorella M.D., Burn T.C., Pratta M.A., Abbazade I., Hollis J.M., Liu R.-Q., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R., Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R., Nagase H., Itoh Y., Ellis D.M., Ross H., Mswail B.H., Murphy K., Hillman M.C. Jr., Hollis G.F., Newton R.C., Magolda R.L.;  
RA "Purification and cloning of aggrecanase-1: a member of the ADAMTS family of proteases.";  
RT Science 284:1664-1666(1999).  
[3]  
RP SEQUENCE FROM N.A.  
RA Sawaji Y., Nagase H., Sakaiyama J., Clark A.R.;  
RT "ADAMTS-4 genomic locus.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
[4]  
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.  
RX MEDLINE=20400518; PubMed=10827174; DOI=10.1074/jbc.M001065200;  
RA Tortorella M.D., Pratta M.A., Liu R.-Q., Abbazade I., Ross H., Burn T.C., Arner E.C.;  
RT "The thrombospondin motif of aggrecanase-1 (ADAMTS-4) is critical for aggrecan substrate recognition and cleavage.";  
RL J. Biol. Chem. 275:25791-25797(2000).  
CC -FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. May play an important role in the destruction of aggrecan in arthritic diseases. Could also be a critical factor in the exacerbation of neurodegeneration in

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OM protein - protein search, using sw model

Run on: November 3, 2005, 08:19:43 (Search time 41 Seconds)

(without alignments)  
1241.431 Million cell updates/sec

Title: US-10-628-432-32

Sequence: 1 MSQTSHPGRGLAGRWLMGA.....DQLDFNIPQAVYKDDDK 529

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

PIR 79:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2801	98.0	837	2	T00355
2	1222	42.7	951	2	T00017
3	706.5	24.7	2165	2	T21371
4	479.5	16.8	1205	2	T18517
5	436.5	15.3	550	2	T47158
6	277.5	9.7	860	2	T16892
7	277.5	9.7	1444	2	T18856
8	268.5	9.4	903	2	S60257
9	250	8.7	480	1	A30065
10	236.5	8.3	407	2	S66260
11	234	8.2	609	2	S55270
12	231.5	8.1	814	2	G02390
13	230	8.0	478	2	A43296
14	227.5	8.0	478	2	J01301
15	225.5	7.9	571	2	S24789
16	224	7.8	616	2	A55796
17	221.5	7.7	478	2	A54880
18	221	7.7	481	2	JC4342
19	218.5	7.6	549	2	S48169
20	217.5	7.6	419	2	S41607
21	217	7.6	481	2	S43125
22	214.5	7.5	414	1	HYRSAC
23	214	7.5	617	2	S48160
24	211.5	7.4	411	1	HYSNRA
25	210.5	7.4	414	2	S41609
26	210	7.3	508	2	T22836
27	207.5	7.3	826	2	A60385
28	200	7.0	484	2	JC8020
29	199.5	7.0	610	2	JC7530

30	193.5	6.8	414	2	S41608	atrolysin B (EC 3.
31	192.5	6.7	610	2	JC8056	halyasee - Glycidu
32	192.5	6.7	655	2	JC7850	disintegrin and me
33	185.5	6.5	429	2	A42972	coagulation factor
34	183.5	6.4	952	2	T18900	disintegrin and me
35	174.5	6.1	957	2	T15976	hypothetical prote
36	172	6.0	670	2	I65967	disintegrin-like m
37	171	6.0	789	2	S28259	androgen-regulated
38	170.5	6.0	419	2	A59414	metalloproteinase
39	167	5.8	524	2	S38539	disintegrin-like m
40	167	5.8	660	2	S71949	metalloproteinase
41	164.5	5.8	905	2	S55059	disintegrin-like m
42	164	5.7	200	2	S15111	metalloproteinase
43	164	5.7	203	2	A59421	fertilin alpha-1 -
44	163	5.7	825	2	A55060	hemorrhagic factor
45	156	5.5	416	2	A37877	metalloproteinase
						fertilin alpha-11
						hemorrhagic protei

#### ALIGNMENTS

##### RESULT 1

T00355 hypothetical protein KIAA0688 - human

C/Species: Homo sapiens (man)

C/Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004

C/Accession: T00355

R:Richikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N

DNA Res. 5, 169-176, 1998

A/Title: Prediction of the coding sequences of unidentified human genes. X. The complet

A/Reference number: Z14142; MUID:98403880; PMID:9734811

A/Accession: T00355

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-837 <1SH>

A/Cross-references: UNIPROT:075173; EMBL:AB014588; NID:93327189; PIDN:BAA1663.1; PID:G

A/Experimental source: brain

C/Genetics:

A/Gene: KIAA0688

F:519-575/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match	Best Local Similarity	Score	2801; DB 2;	Length	837;
Matches	518;	Conservative	1;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	1	MSQTSHPGRGLAGRWLMGAOPCLLPVPLSMVLVLLLASLPSARLASPLPREEE	60		
DB	1	MSQTSHPGRGLAGRWLMGAOPCLLPVPLSMVLVLLLASLPSARLASPLPREEE	60		
QY	61	IVFEKLSGVSPLPGSGTPARLLCRLOAFGETLLLEEDSGVQVEGLTVQYLGQAFELG	120		
DB	61	IVFEKLSGVSPLPGSGTPARLLCRLOAFGETLLLEEDSGVQVEGLTVQYLGQAFELG	120		
QY	121	GAEPQTVLTGTINGDPESVASLHMDGALLGVLOVRGAELHLOPLEGTPNSAGPGAH	180		
DB	121	GABPQTVLTGTINGDPESVASLHMDGALLGVLOVRGAELHLOPLEGTPNSAGPGAH	180		
QY	181	LRRKSPASGQPMCNVAPLPGSPRRPRARAFSLSFVETLVVADDKMAAFHAGLKR	240		
DB	181	LRRKSPASGQPMCNVAPLPGSPRRPRARAFSLSFVETLVVADDKMAAFHAGLKR	240		
QY	241	YLLVMAAAAFHGRPSIRNPVSLVYTRLVLSGSEBGPQVPSAQTLSFCACWQGLN	300		
DB	241	YLLVMAAAAFHGRPSIRNPVSLVYTRLVLSGSEBGPQVPSAQTLSFCACWQGLN	300		
QY	301	TPEDSDPDHPTALLFRQDLGVSCTDTGMAVGTVCDBPASCATVEDDGLQSAFTAA	360		
DB	301	TPEDSDPDHPTALLFRQDLGVSCTDTGMAVGTVCDBPASCATVEDDGLQSAFTAA	360		
QY	361	HQGHVNTMLHNSKPCISLNGPLSTRHVAAPMAHVDDEEPPSPCSARFITDPLNGY	420		
DB	361	HELGHVNTMLHNSKPCISLNGPLSTRHVAAPMAHVDDEEPPSPCSARFITDPLNGY	420		

OM protein - protein search, using bw model

Run on: November 3, 2005, 08:15:58 (Search time 165 Seconds  
(without alignments)  
1239.977 Million cell updates/sec

Title: US-10-628-432-32

Sequence: 1 MSQTGSHPRGLAGRLWLMGA.....DQLQDFNIPQAVDYKDDDDK 529

Scoring table: BLASTN62  
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: geneseqp19808:.\*  
2: geneseqp19908:.\*  
3: geneseqp20008:.\*  
4: geneseqp20018:.\*  
5: geneseqp20028:.\*  
6: geneseqp20038:.\*  
7: geneseqp20038:.\*  
8: geneseqp20048:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2859	100.0	529	8	ADS20235 Human ags
2	2821.5	98.7	584	8	ADS20234 Human ags
3	2808	98.2	846	8	ADS20232 Human ags
4	2805	98.1	686	8	ADS20229 Human ags
5	2805	98.1	697	8	ADS20227 Human ags
6	2805	98.1	837	2	AAW75425 Human ags
7	2805	98.1	837	7	ADJ69542 Human ags
8	2805	98.1	837	8	ADS20209 Human ags
9	2804	98.1	845	8	ADS20243 Human ags
10	2801	98.0	520	7	ADB85490 Human ags
11	2801	98.0	575	7	ADB85489 Human ags
12	2801	98.0	837	7	AAAG78228 Human ags
13	2801	98.0	837	7	ADB85488 Human ags
14	2801	98.0	840	3	AAAB21256 Human ags
15	2798	97.9	837	3	AAAY99429 Human PRO
16	2798	97.9	837	3	AAAB61178 Human PRO
17	2798	97.9	837	4	AAU29199 Human PRO
18	2798	97.9	837	4	AAU29199 Human PRO
19	2798	97.9	837	6	ABU58575 Human PRO
20	2798	97.9	837	6	ABU84438 Human PRO
21	2798	97.9	837	6	ABR66312 Human hum
22	2798	97.9	837	6	ABR65702 Human sec
23	2798	97.9	837	6	ABU96442 Human sec
24	2798	97.9	837	6	ABU82881 Human PRO
25	2798	97.9	837	6	ABU90002 Novel hum

26	2798	97.9	837	6	ABR68251 Human sec
27	2798	97.9	837	6	ABU96304 Novel hum
28	2798	97.9	837	6	ABU92735 Human sec
29	2798	97.9	837	6	ABO08812 Human sec
30	2798	97.9	837	6	ABO02864 Human sec
31	2798	97.9	837	6	ABR75018 Human sec
32	2798	97.9	837	6	ABR94780 Human sec
33	2798	97.9	837	6	ABU85753 Human PRO
34	2798	97.9	837	6	ABU98913 Human PRO
35	2798	97.9	837	6	ABU98128 Human PRO
36	2798	97.9	837	6	ABU91834 Human hum
37	2798	97.9	837	6	ABU89527 Human hum
38	2798	97.9	837	6	ABU86368 Human PRO
39	2798	97.9	837	6	ABU86368 Human PRO
40	2798	97.9	837	6	ABU86069 Human PRO
41	2798	97.9	837	6	ABR9527 Human PRO
42	2798	97.9	837	6	ABR9527 Human PRO
43	2798	97.9	837	6	ABO16440 Human sec
44	2798	97.9	837	6	ABR92340 Human sec
45	2798	97.9	837	6	ABO18981 Human sec

ALIGNMENTS

RESULT 1	ADS20235	standard; protein; 529 AA.
ID	ADS20235	
XX	ADS20235	
AC	ADS20235	
DT	18-NOV-2004	(first entry)
DE	Human aggreccanase ADAMTS4 truncated/mutant E362Q protein with FLAG tag 2.	
XX	ADAMTS4; a disintegrin-like and metalloprotease;	
XX	thrombospondin type 1 motif 4; repolysin; zinc metalloprotease;	
KW	aggreccanase; osteopontin; antiinflammatory; antiarthritic; antineumatic;	
KW	cytochrome; osteoarthritis; glioma; cancer; inflammatory joint;	
KW	rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease;	
KW	human; enzyme; chromosome 1q21-q23; truncation; FLAG tag; mutant; mutein.	
XX		
OS	Homo sapiens.	
XX	Synthetic.	
FT	Misc-difference 362	Location/Qualifiers
FT	Misc-difference 521..529	/note="Wild-type Glu substituted by Gln"
FT	Misc-difference 521..529	/note="Wild-type residues 521-837 replaced by FLAG tag"
XX	MO2004011637-A2.	
PD	05-FEB-2004.	
XX		
PF	29-JUL-2003; 2003WO-US023484.	
PR	29-JUL-2002; 2002US-0398721P.	
XX		
PA	(AMHP) WYETH.	
PA	(CORC) CORCORAN C J.	
PA	(PLAN) FLANNERY C R.	
PA	(ZENG) ZENG W.	
PA	(BACT) RACIE L A.	
PA	(MCDON) MCDONAGH T.	
PA	(FREE) FREEMAN B A.	
PA	(GEOR) GEORGIADIS K E.	
XX	(LAVA) LAVALLIE E R.	
XX		
PI	Corcoran C J, Flannery C R, Zeng W, Racie L A, Mcdonagh T;	
PI	Freeman B A, Georgiadis K E, Lavallie E R;	
XX		
DR	WPI; 2004-143860/14.	

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OM protein - protein search, using SW model

Run on: November 3, 2005, 08:20:33 (Search time 42 Seconds  
(without alignments)  
940.223 Million cell updates/sec

Title: US-10-628-432-32  
Perfect score: 2859  
Sequence: 1 MSQTSHPGRGLAGRLMGA.....DQIDFNIPQAVDYKDDDK 529

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

- 1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2805	98.1	837	4	US-09-122-126B-2
2	2805	98.1	837	4	US-09-634-286A-2
3	2805	98.1	837	4	US-10-247-685-2
4	1222	42.7	950	4	US-09-321-987B-4
5	1193	41.7	967	4	US-09-130-491-2
6	1189	41.6	949	4	US-09-568-559-2
7	1097	38.4	950	4	US-10-009-332-1
8	1050	36.7	727	4	US-09-445-023A-12
9	1046.5	36.6	727	4	US-09-445-023A-12
10	1011.5	35.4	905	3	US-09-369-364A-9
11	852.5	29.8	608	4	US-09-130-491-13
12	837.5	29.3	930	3	US-09-369-364A-15
13	827	28.9	930	4	US-09-122-126B-15
14	827	28.9	930	4	US-09-634-286A-15
15	827	28.9	930	4	US-09-369-364A-15
16	783.5	27.4	1882	3	US-09-369-364A-13
17	733	25.6	874	3	US-09-369-364A-15
18	717	25.1	2150	4	US-09-321-987B-2
19	706.5	24.7	2165	4	US-09-800-729-155
20	645.5	22.6	997	3	US-09-369-364A-11
21	636	22.2	245	3	US-09-369-364A-11
22	592	20.7	589	4	US-09-663-791-12
23	592	20.7	908	4	US-09-663-791-12
24	574	20.1	1104	4	US-09-981-953A-4
25	559.5	19.6	438	4	US-09-663-791-22
26	559.5	19.6	757	4	US-09-663-791-24
27	544.5	19.0	507	4	US-09-963-791-10

28	512	17.9	356	4	US-09-963-791-20	Sequence 20, Appl
29	505.5	17.7	1224	4	US-09-930-872-4	Sequence 4, Appl
30	505.5	17.7	1224	4	US-10-217-774-4	Sequence 4, Appl
31	485.5	17.0	1211	4	US-09-949-016-11401	Sequence 11401, A
32	479.5	16.8	969	4	US-09-321-987B-5	Sequence 5, Appl
33	479.5	16.8	1211	4	US-09-491-522-5	Sequence 7, Appl
34	468.5	16.4	566	4	US-09-949-016-7010	Sequence 7010, Ap
35	468.5	16.4	566	4	US-09-949-016-8505	Sequence 8505, Ap
36	467	16.3	566	4	US-09-481-522-7	Sequence 7, Appl
37	451	15.8	468	4	US-09-963-791-6	Sequence 6, Appl
38	449	15.7	1081	3	US-09-369-364A-17	Sequence 17, Appl
39	448.5	15.7	1205	4	US-09-491-522-11	Sequence 11, Appl
40	435.5	15.2	551	4	US-09-130-491-16	Sequence 16, Appl
41	426	14.9	859	3	US-09-369-364A-5	Sequence 5, Appl
42	424.5	14.8	353	4	US-09-270-767-32624	Sequence 32624, A
43	418.5	14.6	317	4	US-09-963-791-16	Sequence 16, Appl
44	403.5	14.1	1039	4	US-09-949-016-7859	Sequence 7859, Ap
45	358	12.5	491	4	US-09-930-872-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-09-122-126B-2  
Sequence 2, Application US/09122126B  
Patent No. 6451575  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES  
FILE REFERENCE: DM6909  
CURRENT APPLICATION NUMBER: US/09/122,126B  
CURRENT FILING DATE: 1998-07-24  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 837  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-122-126B-2

Query Match 98.1% Score 2805; DB 4; Length 837;  
Best Local Similarity 99.8% Pred. No. 2.1e-245;  
Matches 519; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSQTSHPGRGLAGRLMGAQPCLLPVPLSWMLLLLLASLLPSARLASPLPREB	60
DB	1	MSQTSHPGRGLAGRLMGAQPCLLPVPLSWMLLLLLASLLPSARLASPLPREB	60
QY	61	IVPEKINGSVLPSSGAPARLLCRLQAFGRTLLLEBDSGVQVEGLTVQYLGAPBELLG	120
DB	61	IVPEKINGSVLPSSGAPARLLCRLQAFGRTLLLEBDSGVQVEGLTVQYLGAPBELLG	120
QY	121	GAERGTYLGTINGDPESVASLHWDGALLGVLYRGAELHLOPLEGGTSPSAGPGANH	180
DB	121	GAERGTYLGTINGDPESVASLHWDGALLGVLYRGAELHLOPLEGGTSPSAGPGANH	180
QY	181	LRRKSPASGGPGMCNVAPLGSPPRRPRAKRFASLSRPVETLVVADKMAAFGAGLKR	240
DB	181	LRRKSPASGGPGMCNVAPLGSPPRRPRAKRFASLSRPVETLVVADKMAAFGAGLKR	240
QY	241	YLLTVAAMAAKAPKHSIRNPVSLVTVTRVYLLSGSGEGPVGSAQTLSFCAMQGLN	300
DB	241	YLLTVAAMAAKAPKHSIRNPVSLVTVTRVYLLSGSGEGPVGSAQTLSFCAMQGLN	300
QY	301	TPEDSDPDHFDYALFTTRQDLGVSTCDPTLGMADVGVCDPARSCAIVEDGLOSAFTAA	360
DB	301	TPEDSDPDHFDYALFTTRQDLGVSTCDPTLGMADVGVCDPARSCAIVEDGLOSAFTAA	360
QY	361	HQGHVFNMLHNSKPCISLNGPLSTRHVMAVPMVAHVDPBEPWSPCSARFITDFLDNGY	420
DB	361	HQGHVFNMLHNSKPCISLNGPLSTRHVMAVPMVAHVDPBEPWSPCSARFITDFLDNGY	420

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:23:29 ; Search time 170 Seconds

(without alignments)  
1301.992 Million cell updates/sec

Title: US-10-628-432-32

Sequence: 1 MSQTSHPGRGLAGRLWLMGA.....DQLQDNFIQAVDYKDDDK 529

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
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22: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2859	100.0	529	16 US-10-628-432-32	Sequence 32, Appl
2	2821.5	98.7	584	16 US-10-628-432-31	Sequence 31, Appl
3	2808	98.2	846	16 US-10-628-432-29	Sequence 29, Appl
4	2805	98.1	686	16 US-10-628-432-26	Sequence 26, Appl
5	2805	98.1	697	16 US-10-628-432-24	Sequence 24, Appl
6	2805	98.1	837	14 US-10-247-685-2	Sequence 2, Appl
7	2805	98.1	837	16 US-10-408-765A-1348	Sequence 1348, Ap
8	2805	98.1	837	16 US-10-628-432-1	Sequence 1, Appl
9	2804	98.1	845	16 US-10-628-432-40	Sequence 40, Appl
10	2801	98.0	520	15 US-10-358-283-13	Sequence 13, Appl
11	2801	98.0	575	15 US-10-358-283-12	Sequence 12, Appl

12	2801	98.0	837	15 US-10-358-283-11	Sequence 11, Appl
13	2798	97.9	837	10 US-09-946-374-317	Sequence 317, App
14	2798	97.9	837	13 US-10-052-586-352	Sequence 352, App
15	2798	97.9	837	14 US-10-174-590-352	Sequence 352, App
16	2798	97.9	837	14 US-10-176-758-352	Sequence 352, App
17	2798	97.9	837	14 US-10-175-737-352	Sequence 352, App
18	2798	97.9	837	14 US-10-174-581-352	Sequence 352, App
19	2798	97.9	837	14 US-10-176-483-352	Sequence 352, App
20	2798	97.9	837	14 US-10-176-483-352	Sequence 352, App
21	2798	97.9	837	14 US-10-176-914-352	Sequence 352, App
22	2798	97.9	837	14 US-10-176-915-352	Sequence 352, App
23	2798	97.9	837	14 US-10-175-706-352	Sequence 352, App
24	2798	97.9	837	14 US-10-175-738-352	Sequence 352, App
25	2798	97.9	837	14 US-10-175-738-352	Sequence 352, App
26	2798	97.9	837	14 US-10-175-749-352	Sequence 352, App
27	2798	97.9	837	14 US-10-176-482-352	Sequence 352, App
28	2798	97.9	837	14 US-10-176-915-352	Sequence 352, App
29	2798	97.9	837	14 US-10-176-915-352	Sequence 352, App
30	2798	97.9	837	14 US-10-180-552-352	Sequence 352, App
31	2798	97.9	837	14 US-10-180-557-352	Sequence 352, App
32	2798	97.9	837	14 US-10-173-700-352	Sequence 352, App
33	2798	97.9	837	14 US-10-174-572-352	Sequence 352, App
34	2798	97.9	837	14 US-10-174-579-352	Sequence 352, App
35	2798	97.9	837	14 US-10-174-582-352	Sequence 352, App
36	2798	97.9	837	14 US-10-174-588-352	Sequence 352, App
37	2798	97.9	837	14 US-10-175-739-352	Sequence 352, App
38	2798	97.9	837	14 US-10-175-740-352	Sequence 352, App
39	2798	97.9	837	14 US-10-175-743-352	Sequence 352, App
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41	2798	97.9	837	14 US-10-176-492-352	Sequence 352, App
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43	2798	97.9	837	14 US-10-176-750-352	Sequence 352, App
44	2798	97.9	837	14 US-10-176-985-352	Sequence 352, App
45	2798	97.9	837	14 US-10-176-992-352	Sequence 352, App

ALIGNMENTS

RESULT 1  
US-10-628-432-32  
Sequence 32, Application US/10628432  
Publication No. US20040142863A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: Modified ADAMTS4 molecules  
FILE REFERENCE: AM101378  
CURRENT FILING DATE: 2003-07-29  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 32  
LENGTH: 529  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Truncated ADAMTS4 ASM  
US-10-628-432-32

Query Match	100.0%	Score 2859;	DB 16;	Length 529;
Best Local Similarity	100.0%	Pred. No. 3.5e-231;		
Matches 529;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSQTSHPGRGLAGRLWLMGAQPCILLIPVLSWTLILLILASLPARLASPLPREE	60	
Db	1	MSQTSHPGRGLAGRLWLMGAQPCILLIPVLSWTLILLILASLPARLASPLPREE	60	
Qy	61	IVPEKMGVSLPGSGAPARLLCRLOAFGFTLLLEBODSGVOVEGLTVQYLGAPSLG	120	
Db	61	IVPEKMGVSLPGSGAPARLLCRLOAFGFTLLLEBODSGVOVEGLTVQYLGAPSLG	120	
Qy	121	GAPGTYLTCTINGDEPSVASLMDGALLGVLOYGAEHLIPLLEGTPNSAGPGANH	180	
Db	121	GAPGTYLTCTINGDEPSVASLMDGALLGVLOYGAEHLIPLLEGTPNSAGPGANH	180	